# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 22:07:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716565.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716565.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 22:07:39 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716565.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,232,734 |
| Mapped reads | 1,135,571 / 92.12% |
| Unmapped reads | 97,163 / 7.88% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 27,360 / 2.22% |
| Read min/max/mean length | 30 / 101 / 101.81 |
| Duplicated reads (estimated) | 40,383 / 3.28% |
| Duplication rate | 2.74% |
| Clipped reads | 1,161,148 / 94.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,433,090 / 25.84% |
| Number/percentage of C's | 17,299,531 / 19.93% |
| Number/percentage of T's | 25,532,439 / 29.41% |
| Number/percentage of G's | 21,548,953 / 24.82% |
| Number/percentage of N's | 3,414 / 0% |
| GC Percentage | 44.75% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0281 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2374 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.44 |

## 2.5. Mismatches and indels

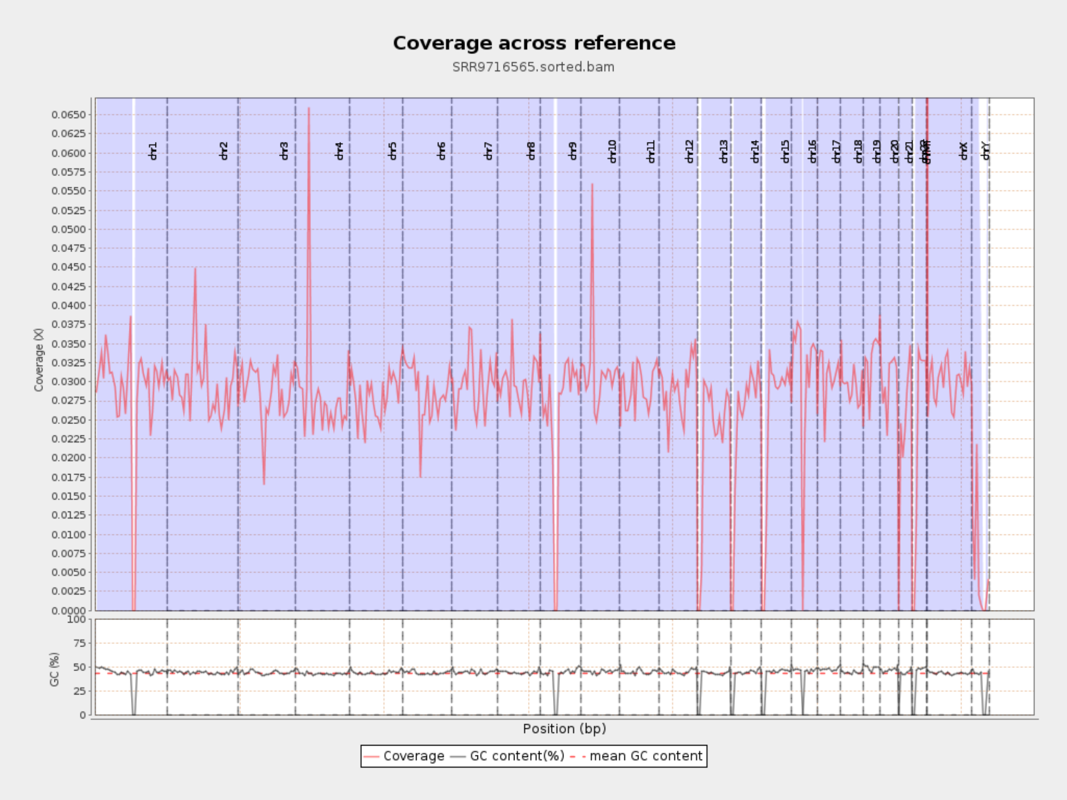
| | |
|---|---|
| General error rate | 0.68% |
| Mismatches | 571,679 |
| Insertions | 7,615 |
| Mapped reads with at least one insertion | 0.66% |
| Deletions | 17,123 |
| Mapped reads with at least one deletion | 1.48% |
| Homopolymer indels | 37.67% |

## 2.6. Chromosome stats

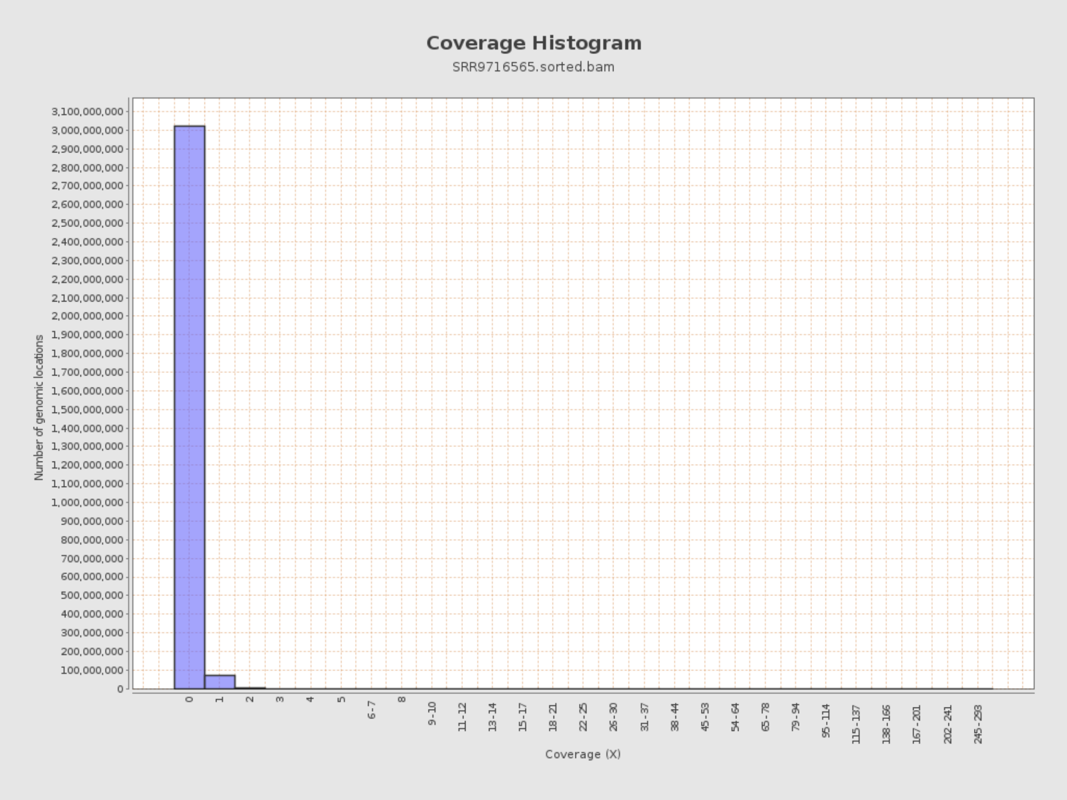
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7115309 | 0.0285 | 0.3058 |
| chr2 | 243199373 | 7234403 | 0.0297 | 0.2679 |
| chr3 | 198022430 | 5688724 | 0.0287 | 0.1872 |
| chr4 | 191154276 | 5497890 | 0.0288 | 0.2601 |
| chr5 | 180915260 | 5096528 | 0.0282 | 0.1846 |
| chr6 | 171115067 | 4920030 | 0.0288 | 0.1957 |
| chr7 | 159138663 | 4729768 | 0.0297 | 0.2796 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4351484 | 0.0297 | 0.2406 |
| chr9 | 141213431 | 3640344 | 0.0258 | 0.2203 |
| chr10 | 135534747 | 4290922 | 0.0317 | 0.3276 |
| chr11 | 135006516 | 3966688 | 0.0294 | 0.2465 |
| chr12 | 133851895 | 3910962 | 0.0292 | 0.1903 |
| chr13 | 115169878 | 2550784 | 0.0221 | 0.1644 |
| chr14 | 107349540 | 2606018 | 0.0243 | 0.1863 |
| chr15 | 102531392 | 2547383 | 0.0248 | 0.174 |
| chr16 | 90354753 | 2742868 | 0.0304 | 0.206 |
| chr17 | 81195210 | 2500014 | 0.0308 | 0.2136 |
| chr18 | 78077248 | 2301864 | 0.0295 | 0.3182 |
| chr19 | 59128983 | 1932743 | 0.0327 | 0.2736 |
| chr20 | 63025520 | 1889538 | 0.03 | 0.2044 |
| chr21 | 48129895 | 1173129 | 0.0244 | 0.222 |
| chr22 | 51304566 | 1173773 | 0.0229 | 0.1713 |
| chrMT | 16571 | 13125 | 0.792 | 1.1294 |
| chrX | 155270560 | 4663216 | 0.03 | 0.205 |
| chrY | 59373566 | 315718 | 0.0053 | 0.2179 |

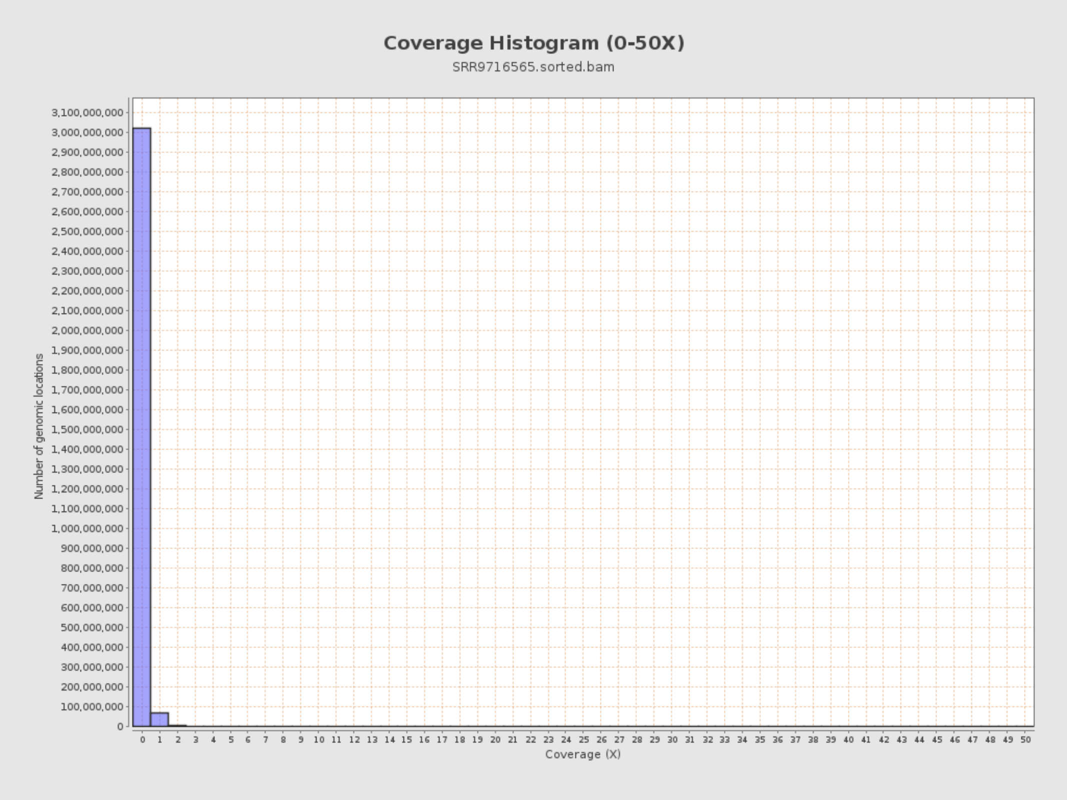
# 3. Results : Coverage across reference



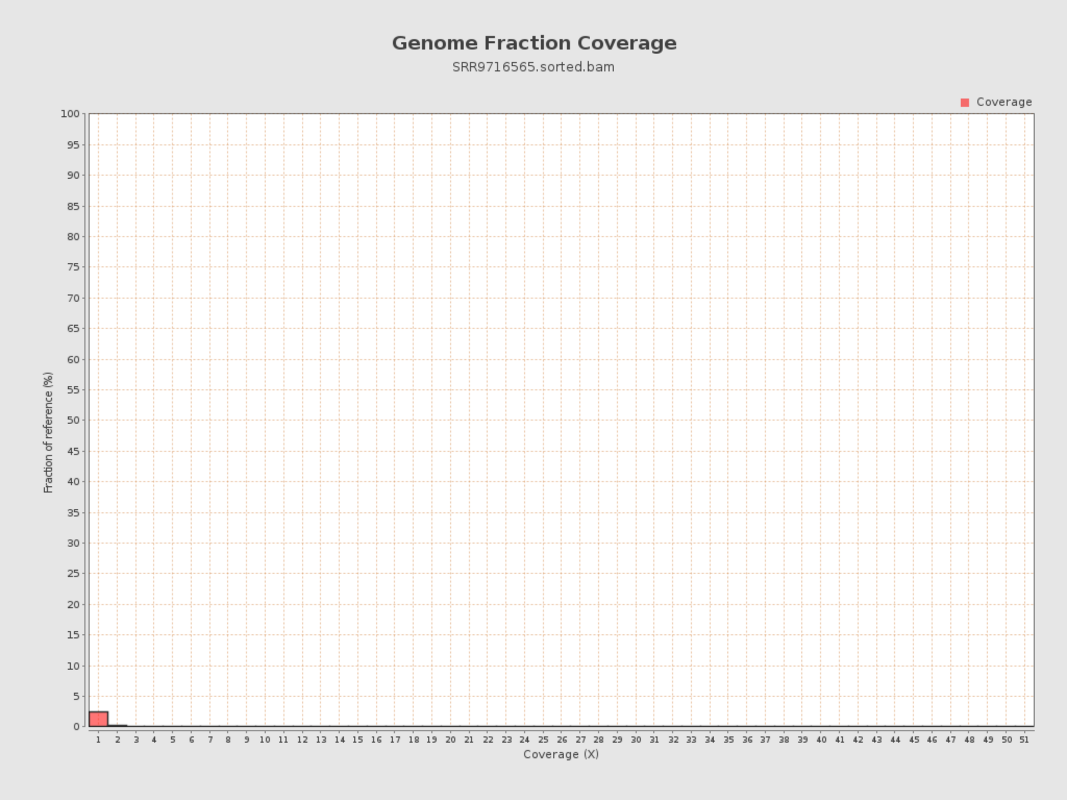
# 4. Results : Coverage Histogram



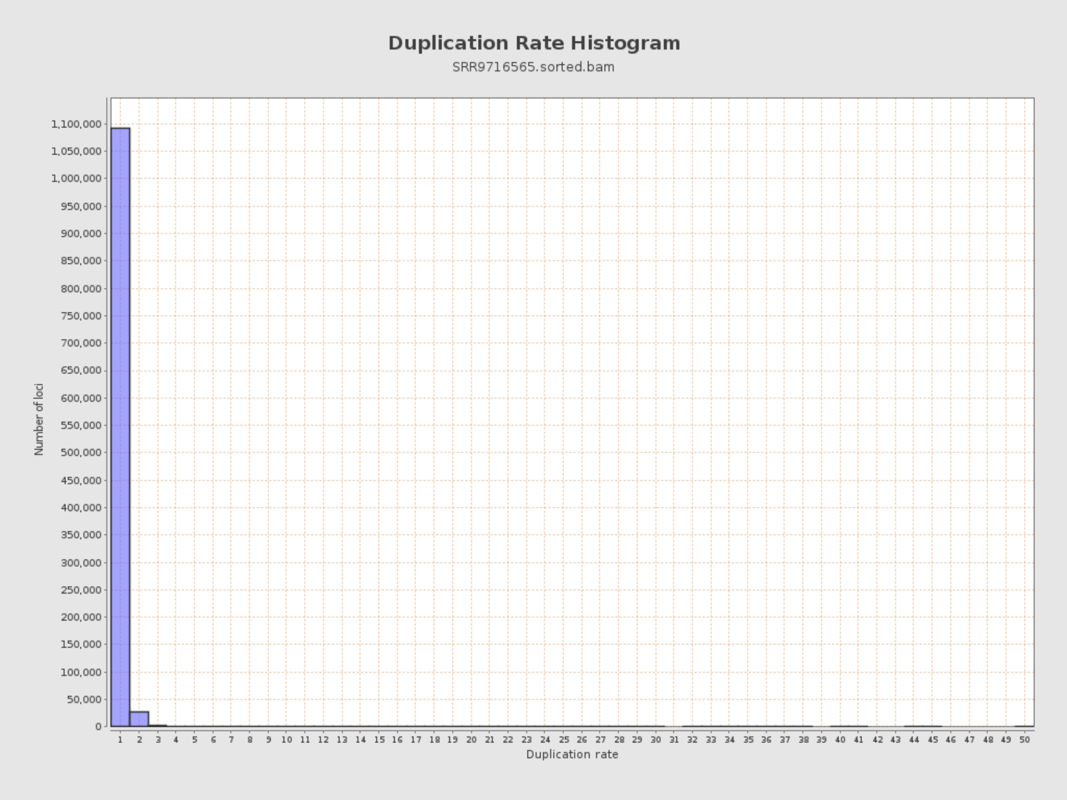
# 5. Results : Coverage Histogram (0-50X)



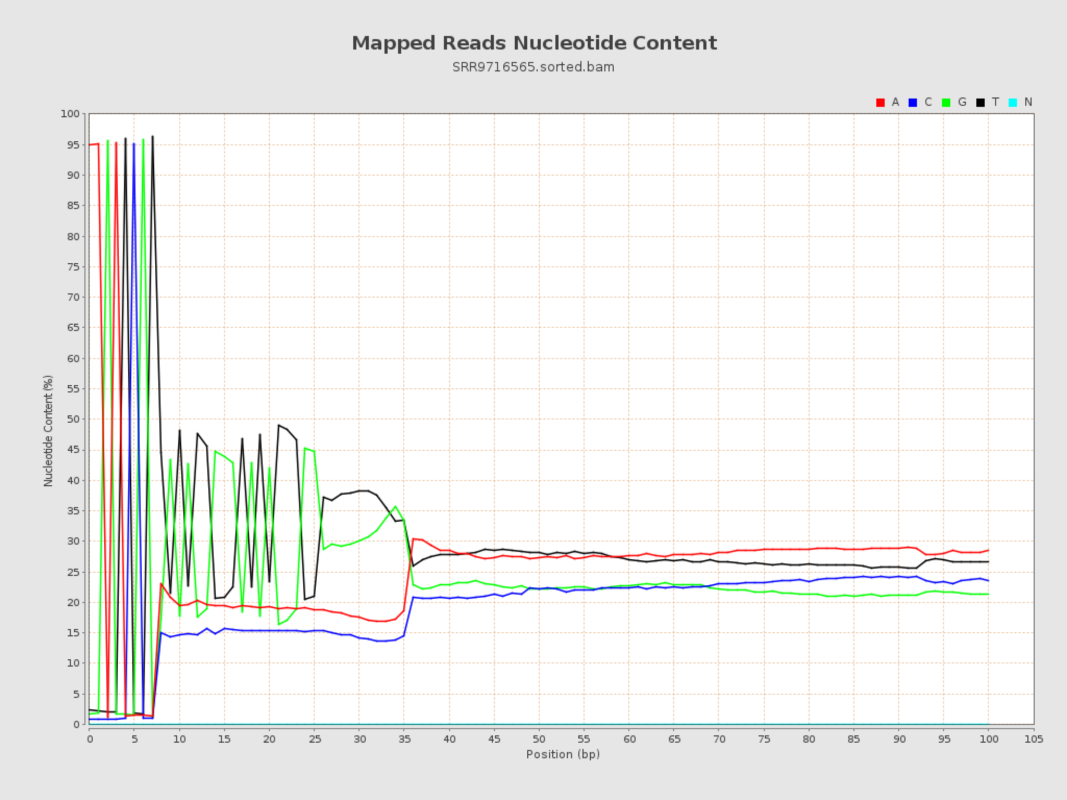
# 6. Results : Genome Fraction Coverage



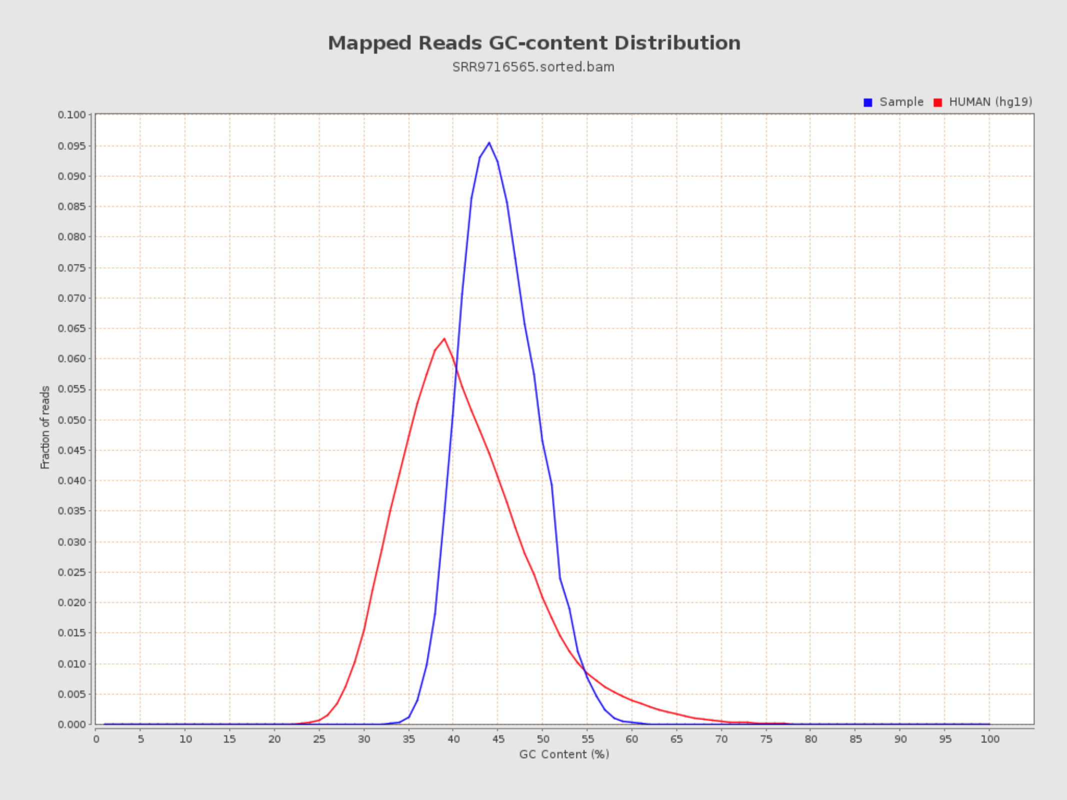
# 7. Results : Duplication Rate Histogram



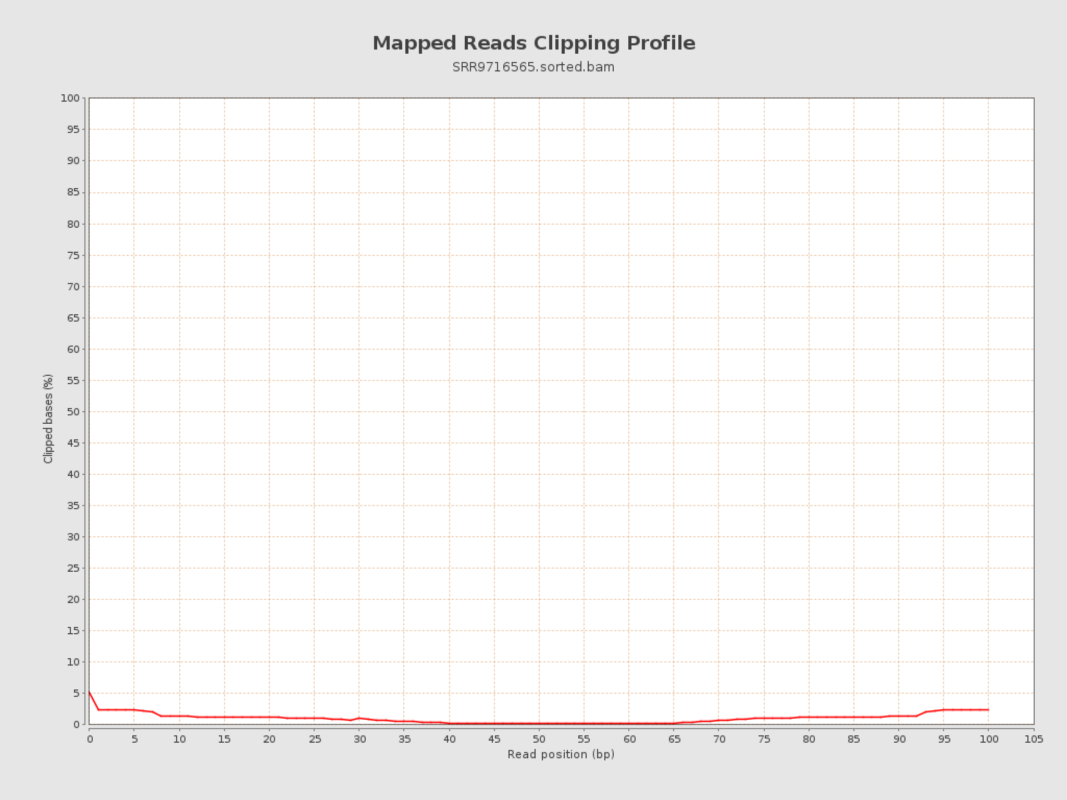
# 8. Results : Mapped Reads Nucleotide Content



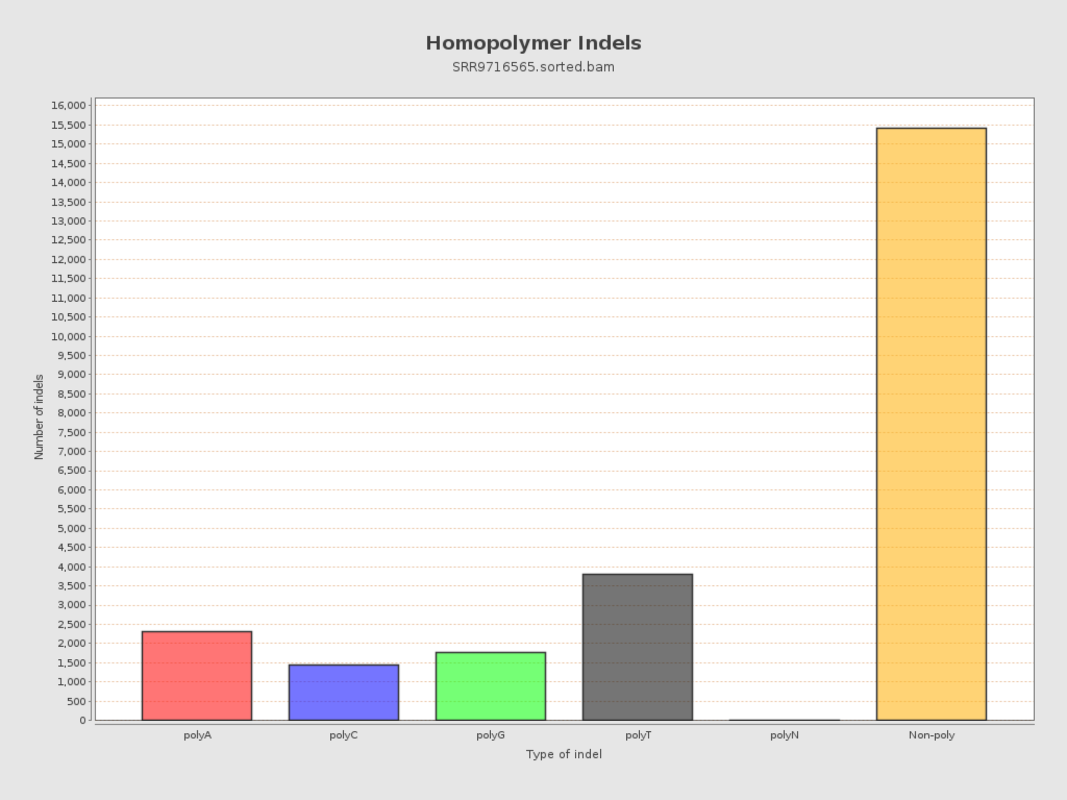
# 9. Results : Mapped Reads GC-content Distribution



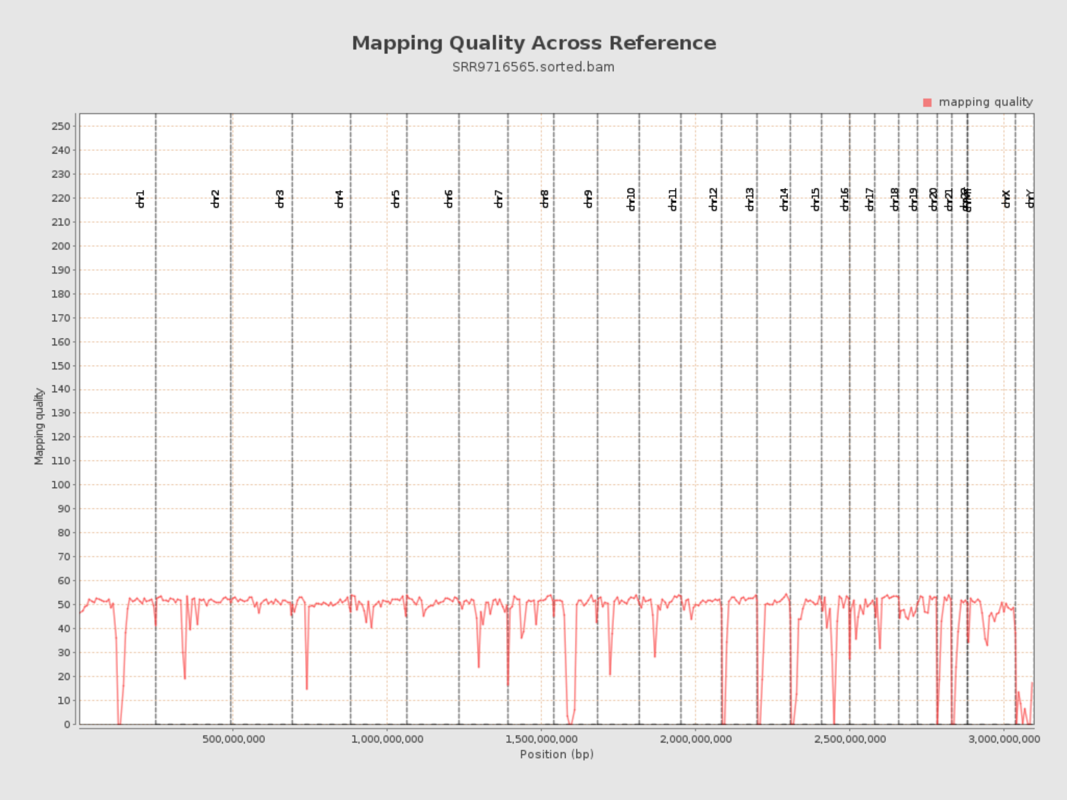
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram